

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/593,015
Source: IFWP
Date Processed by STIC: 10/6/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 10/06/2006

PATENT APPLICATION: US/10/593,015

TIME: 11:20:07

Input Set : F:\Sequence Listing - 13987-00023-US.txt

Output Set: N:\CRF4\10062006\J593015.raw

3 <110> APPLICANT: Hillebrand, Helke
 4 Ebneith, Marcus
 5 Nasholm, Torgny
 6 Erikson, Oskar
 7 Hertzberg, Magnus
 9 <120> TITLE OF INVENTION: POST HARVEST CONTROL OF GENETICALLY MODIFIED CROP GROWTH
 10 EMPLOYING D-AMINO ACID COMPOUNDS
 12 <130> FILE REFERENCE: 13987-00023-US
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/593,015
 C--> 14 <141> CURRENT FILING DATE: 2006-09-15
 14 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/002735
 15 <151> PRIOR FILING DATE: 2005-03-15
 17 <150> PRIOR APPLICATION NUMBER: EP 04006377.8
 18 <151> PRIOR FILING DATE: 2004-03-17
 20 <160> NUMBER OF SEQ ID NOS: 19
 22 <170> SOFTWARE: PatentIn version 3.3
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1160
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Rhodosporidium toruloides
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(1104)
 32 <223> OTHER INFORMATION: coding for DAAO
 34 <400> SEQUENCE: 1
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 36 Met His Ser Gln Lys Arg Val Val Val Leu Gly Ser Gly Val Ile Gly
 37 1 5 10 15
 38 ctg agc agc gcc ctc atc ctc gct cgg aag ggc tac agc gtg cat att 96
 39 Leu Ser Ser Ala Leu Ile Leu Ala Arg Lys Gly Tyr Ser Val His Ile
 40 20 25 30
 41 ctc gcg cgc gac ttg ccg gag gac gtc tcg agc cag act ttc gct tca 144
 42 Leu Ala Arg Asp Leu Pro Glu Asp Val Ser Ser Gln Thr Phe Ala Ser
 43 35 40 45
 44 cca tgg gct ggc gcg aat tgg acg cct ttc atg acg ctt aca gac ggt 192
 45 Pro Trp Ala Gly Ala Asn Trp Thr Pro Phe Met Thr Leu Thr Asp Gly
 46 50 55 60
 47 cct cga caa gca aaa tgg gaa gaa tcg act ttc aag aag tgg gtc gag 240
 48 Pro Arg Gln Ala Lys Trp Glu Glu Ser Thr Phe Lys Lys Trp Val Glu
 49 65 70 75 80
 50 ttg gtc ccg acg ggc cat gcc atg tgg ctc aag ggg acg agg cgg ttc 288
 51 Leu Val Pro Thr Gly His Ala Met Trp Leu Lys Gly Thr Arg Arg Phe
 52 85 90 95

see p. 6

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53	gcg	cag	aac	gaa	gac	ggc	ttg	ctc	ggg	cac	tgg	tac	aag	gac	atc	acg	336	
54	Ala	Gln	Asn	Glu	Asp	Gly	Leu	Leu	Gly	His	Trp	Tyr	Lys	Asp	Ile	Thr		
55			100						105					110				
56	cca	aat	tac	cgc	ccc	ctc	cca	tct	tcc	gaa	tgt	cca	cct	ggc	gct	atc	384	
57	Pro	Asn	Tyr	Arg	Pro	Leu	Pro	Ser	Ser	Glu	Cys	Pro	Pro	Gly	Ala	Ile		
58			115					120						125				
59	ggc	gta	acc	tac	gac	acc	ctc	tcc	gtc	cac	gca	cca	aag	tac	tgc	cag	432	
60	Gly	Val	Thr	Tyr	Asp	Thr	Leu	Ser	Val	His	Ala	Pro	Lys	Tyr	Cys	Gln		
61			130					135						140				
62	tac	ctt	gca	aga	gag	ctg	cag	aag	ctc	ggc	gcg	acg	ttt	gag	aga	cgg	480	
63	Tyr	Leu	Ala	Arg	Glu	Leu	Gln	Lys	Leu	Gly	Ala	Thr	Phe	Glu	Arg	Arg		
64	145					150					155				160			
65	acc	gtt	acg	tcg	ctt	gag	cag	gcg	ttc	gac	ggg	gag	gat	ttg	gtg	gtc	528	
66	Thr	Val	Thr	Ser	Leu	Glu	Gln	Ala	Phe	Asp	Gly	Ala	Asp	Leu	Val	Val		
67					165					170				175				
68	aac	gct	acg	gga	ctt	ggc	gcc	aag	tcg	att	gag	ggc	atc	gac	gac	caa	576	
69	Asn	Ala	Thr	Gly	Leu	Gly	Ala	Lys	Ser	Ile	Ala	Gly	Ile	Asp	Asp	Gln		
70			180						185					190				
71	gcc	gcc	gag	cca	atc	cgc	ggg	caa	acc	gtc	ctc	gtc	aag	tcc	cca	tgc	624	
72	Ala	Ala	Glu	Pro	Ile	Arg	Gly	Gln	Thr	Val	Leu	Val	Lys	Ser	Pro	Cys		
73			195					200						205				
74	aag	cga	tgc	acg	atg	gac	tcg	tcc	gac	ccc	gct	tct	ccc	gcc	tac	atc	672	
75	Lys	Arg	Cys	Thr	Met	Asp	Ser	Ser	Asp	Pro	Ala	Ser	Pro	Ala	Tyr	Ile		
76		210					215					220						
77	att	ccc	cga	cca	ggg	ggc	gaa	gtc	atc	tgc	ggc	ggg	acg	tac	ggc	gtg	720	
78	Ile	Pro	Arg	Pro	Gly	Gly	Glu	Val	Ile	Cys	Gly	Gly	Thr	Tyr	Gly	Val		
79	225					230					235				240			
80	gga	gac	tgg	gac	ttg	tct	gtc	aac	cca	gag	acg	gtc	cag	cgg	atc	ctc	768	
81	Gly	Asp	Trp	Asp	Leu	Ser	Val	Asn	Pro	Glu	Thr	Val	Gln	Arg	Ile	Leu		
82					245					250				255				
83	aag	cac	tgc	ttg	cgc	ctc	gac	ccg	acc	atc	tcg	agc	gac	gga	acg	atc	816	
84	Lys	His	Cys	Leu	Arg	Leu	Asp	Pro	Thr	Ile	Ser	Ser	Asp	Gly	Thr	Ile		
85			260						265					270				
86	gaa	ggc	atc	gag	gtc	ctc	cgc	cac	aac	gtc	ggc	ttg	cga	cct	gca	cga	864	
87	Glu	Gly	Ile	Glu	Val	Leu	Arg	His	Asn	Val	Gly	Leu	Arg	Pro	Ala	Arg		
88			275					280						285				
89	cga	ggc	gga	ccc	cgc	gtt	gag	gca	gaa	cgg	atc	gtc	ctg	cct	ctc	gac	912	
90	Arg	Gly	Gly	Pro	Arg	Val	Glu	Ala	Glu	Arg	Ile	Val	Leu	Pro	Leu	Asp		
91		290					295					300						
92	cgg	aca	aag	tcg	ccc	ctc	tcg	ctc	ggc	agg	ggc	agc	gca	cga	gag	gag	960	
93	Arg	Thr	Lys	Ser	Pro	Leu	Ser	Leu	Gly	Arg	Gly	Ser	Ala	Arg	Ala	Ala		
94	305					310					315				320			
95	aag	gag	aag	gag	gtc	acg	ctt	gtg	cat	gag	tat	ggc	ttc	tcg	agt	gag	1008	
96	Lys	Glu	Lys	Glu	Val	Thr	Leu	Val	His	Ala	Tyr	Gly	Phe	Ser	Ser	Ala		
97					325					330				335				
98	gga	tac	cag	cag	agt	tgg	ggc	gag	gag	gat	gtc	gag	cag	ctc	gtc		1056	
99	Gly	Tyr	Gln	Gln	Ser	Trp	Gly	Ala	Ala	Glu	Asp	Val	Ala	Gln	Leu	Val		
100					340					345				350				
101	gac	gag	gag	gag	ttc	cag	cgg	tac	cac	ggc	gag	gag	cgg	gag	tcg	aag	ttg	1104

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102 Asp Glu Ala Phe Gln Arg Tyr His Gly Ala Ala Arg Glu Ser Lys Leu
103          355          360          365
104 tagggcgggga tttgtggctg tattgcgggc atctacaaga aaaaaaaaaa aaaaaa      1160
106 <210> SEQ ID NO: 2
107 <211> LENGTH: 368
108 <212> TYPE: PRT
109 <213> ORGANISM: Rhodosporidium toruloides
111 <400> SEQUENCE: 2
112 Met His Ser Gln Lys Arg Val Val Val Leu Gly Ser Gly Val Ile Gly
113 1          5          10          15
114 Leu Ser Ser Ala Leu Ile Leu Ala Arg Lys Gly Tyr Ser Val His Ile
115          20          25          30
116 Leu Ala Arg Asp Leu Pro Glu Asp Val Ser Ser Gln Thr Phe Ala Ser
117          35          40          45
118 Pro Trp Ala Gly Ala Asn Trp Thr Pro Phe Met Thr Leu Thr Asp Gly
119          50          55          60
120 Pro Arg Gln Ala Lys Trp Glu Glu Ser Thr Phe Lys Lys Trp Val Glu
121 65          70          75          80
122 Leu Val Pro Thr Gly His Ala Met Trp Leu Lys Gly Thr Arg Arg Phe
123          85          90          95
124 Ala Gln Asn Glu Asp Gly Leu Leu Gly His Trp Tyr Lys Asp Ile Thr
125          100          105          110
126 Pro Asn Tyr Arg Pro Leu Pro Ser Ser Glu Cys Pro Pro Gly Ala Ile
127          115          120          125
128 Gly Val Thr Tyr Asp Thr Leu Ser Val His Ala Pro Lys Tyr Cys Gln
129          130          135          140
130 Tyr Leu Ala Arg Glu Leu Gln Lys Leu Gly Ala Thr Phe Glu Arg Arg
131 145          150          155          160
132 Thr Val Thr Ser Leu Glu Gln Ala Phe Asp Gly Ala Asp Leu Val Val
133          165          170          175
134 Asn Ala Thr Gly Leu Gly Ala Lys Ser Ile Ala Gly Ile Asp Asp Gln
135          180          185          190
136 Ala Ala Glu Pro Ile Arg Gly Gln Thr Val Leu Val Lys Ser Pro Cys
137          195          200          205
138 Lys Arg Cys Thr Met Asp Ser Ser Asp Pro Ala Ser Pro Ala Tyr Ile
139          210          215          220
140 Ile Pro Arg Pro Gly Gly Glu Val Ile Cys Gly Gly Thr Tyr Gly Val
141 225          230          235          240
143 Gly Asp Trp Asp Leu Ser Val Asn Pro Glu Thr Val Gln Arg Ile Leu
144          245          250          255
145 Lys His Cys Leu Arg Leu Asp Pro Thr Ile Ser Ser Asp Gly Thr Ile
146          260          265          270
147 Glu Gly Ile Glu Val Leu Arg His Asn Val Gly Leu Arg Pro Ala Arg
148          275          280          285
149 Arg Gly Gly Pro Arg Val Glu Ala Glu Arg Ile Val Leu Pro Leu Asp
150          290          295          300
151 Arg Thr Lys Ser Pro Leu Ser Leu Gly Arg Gly Ser Ala Arg Ala Ala
152 305          310          315          320
153 Lys Glu Lys Glu Val Thr Leu Val His Ala Tyr Gly Phe Ser Ser Ala

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154          325          330          335
155 Gly Tyr Gln Gln Ser Trp Gly Ala Ala Glu Asp Val Ala Gln Leu Val
156          340          345          350
157 Asp Glu Ala Phe Gln Arg Tyr His Gly Ala Ala Arg Glu Ser Lys Leu
158          355          360          365
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161 <211> LENGTH: 1005
162 <212> TYPE: DNA
163 <213> ORGANISM: Caenorhabditis elegans
165 <220> FEATURE:
166 <221> NAME/KEY: CDS
167 <222> LOCATION: (1)..(1002)
168 <223> OTHER INFORMATION: coding for DAAO
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171 atg gca aac ata att ccg aag att gca att atc ggc gaa gga gtc att      48
172 Met Ala Asn Ile Ile Pro Lys Ile Ala Ile Ile Gly Glu Gly Val Ile
173 1          5          10          15
174 gga tgt act tca gca ctt caa ata tca aaa gct ata cca aat gcg aaa      96
175 Gly Cys Thr Ser Ala Leu Gln Ile Ser Lys Ala Ile Pro Asn Ala Lys
176          20          25          30
177 ata act gtg ctc cac gat aaa cca ttt aaa aaa tcg tgc agt gca gga      144
178 Ile Thr Val Leu His Asp Lys Pro Phe Lys Lys Ser Cys Ser Ala Gly
179          35          40          45
180 cca gca gga tta ttt aga atc gat tat gag gag aat act gaa tac gga      192
181 Pro Ala Gly Leu Phe Arg Ile Asp Tyr Glu Glu Asn Thr Glu Tyr Gly
182          50          55          60
183 cgt gct tct ttc gcc tgg ttc tca cat ctc tat cgc act aca aaa gga      240
184 Arg Ala Ser Phe Ala Trp Phe Ser His Leu Tyr Arg Thr Thr Lys Gly
185 65          70          75          80
186 tcc gaa acc ggc gtg aaa tta gtt tct gga cat att caa tcc gac aac      288
187 Ser Glu Thr Gly Val Lys Leu Val Ser Gly His Ile Gln Ser Asp Asn
188          85          90          95
189 ttg gag tca ttg aag caa caa caa aga gcc tat ggc gat att gtg tac      336
190 Leu Glu Ser Leu Lys Gln Gln Gln Arg Ala Tyr Gly Asp Ile Val Tyr
191          100          105          110
192 aac ttt aga ttc ttg gat gat aga gaa cgg ctg gac att ttt ccc gaa      384
193 Asn Phe Arg Phe Leu Asp Asp Arg Glu Arg Leu Asp Ile Phe Pro Glu
194          115          120          125
195 cca tca aag cac tgc att cac tac acc gcc tac gca tca gaa ggt aac      432
196 Pro Ser Lys His Cys Ile His Tyr Thr Ala Tyr Ala Ser Glu Gly Asn
197          130          135          140
198 aag tac gtg cct tat ttg aag aat ttg ctg ctt gag caa aaa atc gag      480
199 Lys Tyr Val Pro Tyr Leu Lys Asn Leu Leu Leu Glu Gln Lys Ile Glu
200 145          150          155          160
201 ttc aag caa caa gaa gtg acg agt ttg gac gca gtc gcc gac gct ggt      528
202 Phe Lys Gln Gln Glu Val Thr Ser Leu Asp Ala Val Ala Asp Ala Gly
203          165          170          175
204 tac gat gtt att gta aac tgc gca ggc ttg tac ggt gga aag ttg gct      576
205 Tyr Asp Val Ile Val Asn Cys Ala Gly Leu Tyr Gly Gly Lys Leu Ala

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206          180          185          190
207 ggt gat gac gat act tgc tac ccc att aga gga gtc att ttg gaa gtt      624
208 Gly Asp Asp Asp Thr Cys Tyr Pro Ile Arg Gly Val Ile Leu Glu Val
209          195          200          205
210 gat gca cca tgg cac aag cac ttc aat tat cga gac ttt act act ttc      672
211 Asp Ala Pro Trp His Lys His Phe Asn Tyr Arg Asp Phe Thr Thr Phe
212          210          215          220
213 aca att cca aaa gag cac agc gtg gtg gtt ggg tcc acc aag cag gac      720
214 Thr Ile Pro Lys Glu His Ser Val Val Val Gly Ser Thr Lys Gln Asp
215 225          230          235          240
216 aat cga tgg gat ttg gag atc acc gac gag gat aga aat gat att ttg      768
217 Asn Arg Trp Asp Leu Glu Ile Thr Asp Glu Asp Arg Asn Asp Ile Leu
218          245          250          255
219 aaa cga tac att gct tta cat cct gga atg aga gag cca aag att atc      816
220 Lys Arg Tyr Ile Ala Leu His Pro Gly Met Arg Glu Pro Lys Ile Ile
221          260          265          270
222 aaa gaa tgg tca gca ctt cgc ccg gga cgt aag cat gtc aga att gaa      864
223 Lys Glu Trp Ser Ala Leu Arg Pro Gly Arg Lys His Val Arg Ile Glu
224          275          280          285
225 gcg cag aag agg aca tct gtt gga aac tca aaa gat tat atg gtt gtg      912
226 Ala Gln Lys Arg Thr Ser Val Gly Asn Ser Lys Asp Tyr Met Val Val
227          290          295          300
228 cat cac tat ggt cac ggg agc aac gga ttc acg ttg ggt tgg gga aca      960
229 His His Tyr Gly His Gly Ser Asn Gly Phe Thr Leu Gly Trp Gly Thr
230 305          310          315          320
231 gca att gaa gca act aaa ctt gtt aag act gca cta gga tta taa      1005
232 Ala Ile Glu Ala Thr Lys Leu Val Lys Thr Ala Leu Gly Leu
233          325          330
235 <210> SEQ ID NO: 4
236 <211> LENGTH: 334
237 <212> TYPE: PRT
238 <213> ORGANISM: Caenorhabditis elegans
240 <400> SEQUENCE: 4
241 Met Ala Asn Ile Ile Pro Lys Ile Ala Ile Ile Gly Glu Gly Val Ile
242 1          5          10          15
243 Gly Cys Thr Ser Ala Leu Gln Ile Ser Lys Ala Ile Pro Asn Ala Lys
244          20          25          30
245 Ile Thr Val Leu His Asp Lys Pro Phe Lys Lys Ser Cys Ser Ala Gly
246          35          40          45
247 Pro Ala Gly Leu Phe Arg Ile Asp Tyr Glu Glu Asn Thr Glu Tyr Gly
248          50          55          60
249 Arg Ala Ser Phe Ala Trp Phe Ser His Leu Tyr Arg Thr Thr Lys Gly
250 65          70          75          80
251 Ser Glu Thr Gly Val Lys Leu Val Ser Gly His Ile Gln Ser Asp Asn
252          85          90          95
253 Leu Glu Ser Leu Lys Gln Gln Gln Arg Ala Tyr Gly Asp Ile Val Tyr
254          100          105          110
255 Asn Phe Arg Phe Leu Asp Asp Arg Glu Arg Leu Asp Ile Phe Pro Glu
256          115          120          125

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/593,015

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Input Set : F:\Sequence Listing - 13987-00023-US.txt
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FYI
Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; Xaa Pos. 1,2,4,7,8,9,10,12,13,14,15,16,18

VERIFICATION SUMMARY

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Input Set : F:\Sequence Listing - 13987-00023-US.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1474 M:341 W: (46)' "n" or "Xaa" used, for SEQ ID#:17 after pos.:0

M:341 Repeated in SeqNo=17